

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCGCCATGCGCCTGCCGCCGGCGCTGGGGCTCCTGCCGTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAACGCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACGAAACTTGGCGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGGCAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCCCTGTGGATGTGGACGGAGTGTGCGGCCAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGGAGTGCCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAACG
GAAGATGCCTGTGTGCCGCCAGAGGGCTGAAGGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCTTAAATTATTGAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTCTTA
AACAGACTTGTATATTTGATAACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTAGTTGTGGTTGTCCAAACTC
ATCAAATGTATCTTATCATGTCTGGATCGGAATTAAATTCCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGCGGAAGAACCGAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCAGTC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEARQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLA EKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACTCACCTCGGTTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCAGGGAGGCAGCGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCAGGAGGAGGAGCTGACCTATGGATCGATGCTCACAGGCAAGAGTACTCA
CTGCGCCGCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCGCAGGAGGAGGAGCTGACCTATGGATCGATGCTCACAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCAGGGGGTGGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACGCTCAACCACCTGCTTAAATGGAGGGACC
TGTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCTGCAATGGAGGTAAATGCAATTGGTAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGGTGCACAT
GGAACCTGCCATGAACCCAAACAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
AAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCACTACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCACTGCTTGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCACTGAGCTGAGTGGCAGATATTCAAATACATGCAATTATGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAAGTATTAGAT
GTTTGTACATTTAAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACC
TTACCATTATTCCAGAGATTCACTGAGTATTAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAAATAATGTATGAACCTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACAGCTTACCTAATAAACATTAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAAAAAAAAAAAA
CGCCATGGCCCAACTGTTATTGCAGTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIKSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACCCGTGGCGTCCGGCGTCCGAGAGCCAGGAGGCCAGGGCCGGGGCCAGCCTGGG
CCCCAGCCCACACCTTCAACCAGGGCCAGGAGCCACC**ATG**TGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGTCTGCACCTGCGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCGTCCGACGACTGTGCCCTGCCCTACCTGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGACTTC
TGCCTCGGCGTGCCACCCCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTTGGGAAACGTACTGGACAACGTAACTGTAACCGTTGCACCTGCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCTGG**A**GGGCATTGCTACCGCCTGGCACCA
TCCGCCATCTCCTCGGTATGAAACATGCATGAAATTATAACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCTCTGAGAAGTGGCCAACCTGATTGATGAGCCTTTGA
CCAAGGCAACTGTGCAAGGCTCCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTGCTGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTCGTGC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCAGGCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACATGACATCTACCAAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCAACCTCCTGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGCGTCAATGAGTGCAGATCGAG
AGCTTCTGCTGGCGTCTGGGCCCGTGGCATGGAGGACATGGGTCTCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGCAGGCCAGGGCGCTAAT
CCCAGCGGGTCTCGCTGACGCAGCGCCCGCTGGGAGCCCGGGCAGGGAGACTGGCG
GAGCCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGGAGAGGACAGCTGCAG
ATCCCAGGCCTCTGGGCCCTCAAGACTACAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATAACCCACCCCAATCCGTATTCTTTTTTTAGACAGGGCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCACTCCTGGTTCA
AGTGACCCCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC
TAATTTTGTATTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAAGT
CCTGGCTCAAGCGGTCACCTGCCTCCGCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTTGTAACCCAC
CAGCAGCAGGGCTGCCGCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACGCCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCGCGCAGTTGGCCTCCTGACC GTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCACTGGGAGCCTGTCCTGGTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCGDPASYRLWGAPLQPT
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPFAFSTLNPLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

DRAFT: 2024-02-20

FIGURE 10

CCCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCAGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCAGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGCAGGAGAACAACTATAACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGCCCTCACGCCAGGGCGGCCCGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACAGCAGTCAGTTGAGCTGGCTCCGCCACCCGCCGGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGCCGCGAAGCATCCGAGCCCCCAGCTGGAAAGGGCAGGCCGGTG
CCCCAGGGCGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCAGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGCTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCTCCAGCCCCAAACTCCTCTGGTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCCACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTCTGGACTTCAACAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTCCCACCATGGTATTTAT
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCCACAGGAACTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAAATTAAATATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAAGAATGTCAGAGTTCCATTGCAGGAAAAC
AAATTCAGACCATTTCACGGGCTGCTCTGCCAGCTCTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTCCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCAATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAGAT
AAACACATTCTTGCAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTCAAGGGTTTGATAATTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTGTGACTGCACTTAAATGGTCACAGAATGGCTCAA
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCAAGGTCTGAACAAGTCCGGG
GGATGCCGTAGGAAATTAAATGAATTCTTGTCTGCCCACGACCCCCGGCTG
CCTCTTCACCCAGCCCCAAGTACAGCTCTCCGACCCTCAGCCTCCACCCCTCTCTAT
TCCAACCCTAGCAGAAGCTACACGCCTCAACTCCTACCACATCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCCCACCTATTCTGAACGGATCCAGCTCTATC
CATTTGTGAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA
CAAACTCACATGGGTAAAATGGCCACAGTTAGTAGGGGCATCGTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTACCGCGCGGTAGAAGACACCATTGTCAGAGC
TGTAGTGCCTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTCAGAGC
CACCAACCATGCCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGTCTAGCGTCTTGTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACCGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCACTGTTCAAGTCGTCCTAAATAACGAT
CAACTCCTAAAGGAGATTTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTGCATTGAAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGaffLksWLIISLGLYSQVSkLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTvLYLHNnQINNAGFPAELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHDDNSISTVGVEDGAFREAIslkllflsknHlssVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGnLLTNKGIAEGTFSHLTkLKEFSIVRNslSHPPPD
LPGTHLIRLYLQDNQINHIPLTAfSNLRKLERLDISNNQLRMLTQGVFDNLsNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMcQGPEQVRGMAVRELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTppTPTSKLPTIPDWDRERVTppIseriqlsIHfVND
TSIQVSWLsLFTVMAYKLTWVKMGSLSVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAViFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDnsileMTETsFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGCAGAGGCGACGAGGAAGACCCGGTGGCTCGGCCCTGCC
TCGCTTCCCAGGCAGGCCCTCGCAGCTTGCCCTTGTGCTCGCCTGAAA**ATGGAAAAGATGCTCGCAGGCT**
GCTTCTGCTGATCCTCGAACAGATCGCTCTCCCTGCCAGGGCAGGGCAGGGCAGGTCCATCT
CTAGGGCAGACACGCCCTCGAACACCACCCGAGACGCCCTCTGGAGAGTTCCCTGTGAGAACAAAGCGGGCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGCCTGTGATGTCAACCGAGTGGGGCTGCTCCAATATGGCAGCACTGTCAAGAACATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCGAGGTGGAGCGTGTCAAGAGGAATGCCATCTGTCCACGG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGCCCGCCCTGA
GGGAGAATGTGCCACGGGTCTATAATGATCGTGAACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCTAACTTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGAAGCCCCATGAGGACCATGTCTCTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCGAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTAATGTGCCGGCTCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGACTACTGTGCTCTGAGAAAACACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCGAGTGGACCACTGTGAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACGGAGGATTCTCTGCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCTGCTGAGTGCACATGGTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTGCTGCTAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGAAAGACGTGTG
CAAATGGACTCTTGTGCTCTGGGGGACACGGTTGTGAAACATTGCTGTGTAAGCAGTGAAAGATTGTTGTG
GCCAGTGTGTTGAAGGTTATATCTCCGTGAAGATGGAAAAACCTGCAGAAGGAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAAACACATTGTGTAACAGTGCAGCTCATACACGTGCGAGTGTGTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCAAGGAAGGATGTGCAAATCAACCCACATGGCTGCCAACACATTGTGTTA
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGTGAGGACGGAAGACGGTGAAGAAAAT
GCACTGAAAGGCCAATTGACCTGGTCTTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTG
TGAAGCAGTTGTCACTGGAATTATAGATTCTGACAATTCCCCAAAGCCGCTCGAGTGGGCTGCTCCAGT
ATTCCACACAGGCTCACACAGAGTTCACTCTGAGAAAACCTCAACTCAGGCAAAGACATGAAAAAGCCGTGGCC
ACATGAAATACATGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGACCGAGCCATTGTGTTCACCGACGGACGGCTCAGGATG
ACGTCTCCGAGTGGCCAGTAAAGCCAAGGCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAGCCATTG
AGGAGGAACTACAAGAGATTGCTCTGAGCCCACAAACAAGCATCTCTTATGCCAACAGACTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGCATTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACGTCCAAAACGGTCCAACAGCCAAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGCGAGTGCACACAGATATCTGTTGAAAGAACATCTTACGGTCTACACAAAGCTT
CCCATTCAACAAAACCTCAGGAAGGCCCTTGGAGAAAACACGATCAATGCAAATGTGAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGTAAGAAAATTAAACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATCGCCTGAGATACAGAT**GAAAGATTAGAAATCGCAGACACATTGTAGTCATTGTATCACGGATTACAAT**
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACACTAATTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAAATATACTGTGGACAC
AACTGCTCTGCCTCATCCTGCCATTGTGCAATCTCATTTGACTATACGATAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGCCATAGGAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGGATTAAATACAATATTAAATTACCACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHQPQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAI GVGQVDFNLTKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVADYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGEOLCLNTEDSFVCQCSEGFLI
NEDLKTCRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCALKDSCALGDHGCE
HSCVSSED SFVCQCSEGFLIREDGKTCRVDHCAQQDHGEOLCLNTEDSFVCQCSEGFLI
EDGKRCRKDVCKSTHGCEHICVNNGNSYICKCSEGFLVLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKIAIEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEE DNLRLSTQKLHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCAGGCTGGCGCCCTGACTCCGTCCTGGCCAGGGAGGGC
CATGATTCCCTCCCAGGGCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGTGCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTCGCGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCACAGCATCAAACCT
TAGAACTCAATGTAAGTGGTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCCTGCAATACCA
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGTACCTCTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCACTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGCTCCAGGC
CCCCTGATCTGATCCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAGACTAACATGAAATATGTGTTTTGCAAATTAAAGATAACATAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGGGTTTTCCACTTG
TTGAATTGTTCTATACTCAAATTGACCCAAGACACCTTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATTGAAATGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATTGTCTGTATAGCTGCAAATATTAAATAAAACTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCAATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAAGGCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTACAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTTATATTATA
AGAGTATTGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTCAACTAGGAATAATTATTCAGTATTGTTGCCATATGCATTTT
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGCTG
TAGCCTATTCTTGCTGAACTTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTCATTGTTGGGTGTCACTACAAACAAGGGATTGGCA
CAAGAATTATATCTTGCTATCTAAGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAACAACATT
TGGAGTTTATAGGACCAAGCATGCCTAACTCATTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAAGTTAGTTGCTTGAGAAC
TAAGGTCTTGCAAGAGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTCACGCATCAGGTTACAGCTTACACTCTCACAGTCAGCAATGC
TTCCAGGGATGTTCAATTGTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGCCCCCTGTTGGATGTTAAGGTAACATAGAGAATG
GTGGATAATTACAACGTGACAAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTTATGCTAGGAACACTGTAGATAATAAGGTAATTATGTATCATATAGATAACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCCAAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA
TGTCTGAAGGAAACCACGGCTGATATTCTGTGACTCGTGTGCTTGAAGACTAGTCC
CCTACCACCTCGTAATGAGCTCCATTACAGAAAGTGGACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAAGGAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCAATTGTTGAA
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLP₁LLVVFST₂LLNCSYTQ₃NCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNV₄CIAA
NINKTLTKIRSIKEPVALLQE₅VYRNSVTDSLPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTL₆TEFVKT₇VNNFQRDTFVW₈DKL₉S₁₀VHRRTHL₁₁T₁₂KLMHTVEQATLRISQS₁₃FQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDG₁₄DYINIFPKRKAAYDSNGNVAFLYYK₁₅SIGPLLS
SSDNF₁₆LLKPQNYDNSEEE₁₇ERVISSVISVMS₁₈SNP₁₉TL₂₀YELEK₂₁ITFTLSHRKVTD₂₂RYRS₂₃LC₂₄A₂₅F
WNYSPDTMNGSWSSEGCE₂₆L₂₇TYSNETHTSCRCNHL₂₈THFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA₂₉LG₃₀YRYYGT
TKVCWLSTENNFIWSFIGPA₃₁CL₃₂IILVNLLA₃₃FGV₃₄IIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLF₃₅LLGTTW₃₆IFGVLHV₃₇VHASV₃₈VTAYL₃₉FTVSNAFQGMF₄₀IFLFLCVLSRKI₄₁QEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCAGTGATTTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGCCGCTGCGCGGTGGGAGGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCACCCCGGCTGGGA
CAAGAAGCCGCCGCTGCCCTGCCCGGGCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGC
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGCTCAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTCGCCGAGAGCCCCAGGGAGGTGCCATTGCGAGCGGGTGTGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGGCGGGCGCCCCCTGCCCTCTCGGACGCGGGCC
CCACGTGCACTACGGCTGGGGCAGCCCATTCCGCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTCCTGCGCATCCGTGCGCAGGGCGTGTGGACTGCGCGGGGC
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCGGGACCGTGGCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAAC
GAGACCATGCCGGGCTCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAAGTTCTAGCCAATAGACTTGTCTGAT
CATACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGCAGGAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGATTGATCTATCTCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCA
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCACTGGATGCTGCTGAGAATAACTGCTGCTCCGGTGTACCTGC
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGCCT
CCCAGGCCCCCACCCTATGTCAACCTGCACCTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSQCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESDM
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

100 90 80 70 60 50 40 30 20 10

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAACGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATT
TGTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGTATTCCGTTGTGGCCTGGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTAAAAATGTGCAGTGGCTACGCCTGTAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTTAGACCAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDGEGNPAPEYTWFKDGI
RLLENPRLGSQSTNSSYTMTKTGTLQFNTVSKLDTGEYSCEARN
S VGYRRCPGKRMQVDDLNISGIIIAAVVVVA
LVISVCGLGV CYAQRKG YFSKETSFQKSNSSSKATTMSENV
QWLTPVIPALWKA AAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACACTCCACCTTCAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCTAGTGAAGAAAAACTTTGTGGTTCTATGGCATTCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGTGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCAGGCCAGATTGCC
AGCTAACACACAGATTCTCTCACAGACTAACAAATATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTTGGCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCCTGAAAAATGTCGTCCGAAC TGAGCAACTTACAAGAACTCTATATTAAATCACA
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTATCA
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTCAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATGGTCT
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGATCCGTTG
GATGAACATGAACAAACCAACATTGATGGAGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGTCAAGAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTGT
CTCCCTCTTATAGCTCTGAGAGCTTCTTCTAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAATGGCGTAACTCCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAGAGATATTCAAGGCAATTCACTGTTGGTGTCTGGAAAGCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTCGCAAAGTGTGCAATACCATCTGATGTCAAGGTATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACAACACTTATGGCCTGTCTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDGPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPPLINLRLSLVIAGINLTEIPDNAVLGLENLESISFYDNRL
IKVPHVALQKVVNLKFIDLNKNPINRIRRQDFSNMLHLKELGINNMPELISIDSALVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEDPSLFCVDPPEFQGQNVROVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRAATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**CATGAATCT**
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGAAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**TAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA**
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACACATTGAA
ACTTTGTATTCAGTTTTGGATTATGCCACTGCTGAACCTTAAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACCTTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFMILCFHSASMC PKGCLSSSGGLNVTC SANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNKLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
LNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGAACGAAGGCGCGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGC
GGGCTCAGTGCCTCAGGCTCGGCCACGGCTGCCGCCCCGCTGCAGTGCCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCAGCAAGTGCCTTGAGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGCGCCGGAGGCCGGCG
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTAGGACCTGACAACTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCACTTGGACACCATGACACCCAAC
TGCCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCGCTTCTCAACCTCTCCTACAACCCCATCA
GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGGCCATTGCCTCCGGCCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGTGTCCGG
CGCCGCTGGCCGCTCAACTCAACCGCAGCAGCCCACGTGCGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACACGGTGCAGTT
GTGTGCCGGGCGATGGCAGCCGCCGCCCCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCCAACGCCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGAGCTACTGCCGACTGGCCCCATAGCCAACAA
GACCTCGCTTCATCTCAACAGCCGGCGAGGGAGAGGCCAACAGCACCCGCGCACTG
TGCCCTTCCCTCGACATCAAGACCTCATCATGCCACCACATGGGCTCATCTCTTC
CTGGCGTGTCTCTCTGCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGACAACATCGAGATCGAGTATGTGCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCCGCCGCAAGTTAACATGAAGATGATTGAGGCCGGGCGGGGGCAGGGACCCCCG
GGCGGCCGGGAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCCAGTCCTTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCCTGCTGCCCG
CCAGCCCTACCACCTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTCAATAATTATGGATTT
TATGAAAATGAAATAATAAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKYLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQOV
FVDEGHTVQFVCRADGPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGC
TGTTGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCC
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGG
ATAAAATCTCATTACGGGAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTCC
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGCGGGACACGGCCATCATCAATGCGAGAGGCG
GGCAGTCAGGAGGGACGACAAGGAATATTCATAGAGGCGCTGCCACTTCC
GCCCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTGCTCCCCAGCCACCCACCCCGTACAGAACATGCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCCTTCTTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGGCTGTTGGATTCTGTT
GCTGGAGACGTCTCTTGTGCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCACCTCGACCTCCGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTCGGACCATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA
GCTTTCCACGAGATAACAAGATCCACAGCATCGAAAATCGACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGCTGAAAACACTAGAGTACCTGAACGTGGACTACAACGCTATCCAGCTCA
TCCTCCGGGACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACACCTG
CTGAGGTCCCTGCCTGGACGTGGCTCGCTGGCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCCTGCACAATTGTGCCCTCAAGCAGTGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTAACCTCTT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
GCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGTGTGGTCCGGACTGCTGCTGGT
GTTGTCACCTCCGCCTCACCGTGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GAACCTCCTACTGGCACAAATGGCCTTACAACCGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCCAAATAGGGGAGGGCAGAGGAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTGTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCTGTGGGTTGGATGCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAFTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFQLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLIILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPIGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRIQLQ
GKDLNETTEQDLCPLKNRVDSSLAPPQEEETFAPGPLPTPKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRNVSSLADLKPK
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNYYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSIISVL
VPGLLVFVTSAAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCAGCTGTGTTCTGACCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGTCGGCCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGTCCGTGGGAGCGAGGGCGGAGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGAGCAGCTCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCTCGCCCTGTGCCTCTGGCAGGCCTCTGGCCGGGGCCTGCTACAGCCTGC
CGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCAGGCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGGCGCTGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCACTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTTCTCCTGGCTGTCCTCCGACCCCGGGCGTCTC
GAAAGCGACACGCTGCAAGTGGGAGGCCAACGCTCCTGCACCGCGGGAGATGCG
GGTACTCCAGGCCACCGTGGGTCGAGGCCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCGG
GCCGCTCTAACATTGAGCTATCGCGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGTGGACAAACTCTCGGGGATGTGTTGTGTCCTGCC
GGGAGGTACCTCCGTGGCAAATGCGCAGAGCTCCCTAACGCCTAGACGACTTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCCGCTTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCCAGGCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGCCAATCAGGGTCGACCGAGAACGCTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCACTAACATCTATTCCCTGAGATTCCCTCGATGGGAT
CACAGAGCACCGATGTCTACCCCTCAAATGTCCTCAAGCCAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCCCTGCCACTCCTCAGGCTT
CGACTCCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGTGT
TGACCATGACAGTACTGGGCTGTCAAGCTCTGCTTCAAGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGCCCGCCGGCTGGAGAGGTGATCCTGAGGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGTGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCCTTGGCTCTAGTGTGATGCAT**TAGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGTGATTGAACCTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDILLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCP
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSIQAESKATITP
SGSVISKFNSTTSSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCCCGCCCGGGCGTGCAGCGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGC
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGC
GGGGCGTGTGCGCGCGCGCGTGGGTGCAAACCCGAGCGTCTACGCTGCCCATGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCACCCAGCTCTCGCG
CAGCAGTCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGGCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTCTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCCTACAACACTACAGAACAGCCTGCACCACATTCCCTGTAACCACGGTTAAA
ACCCACCGTGGCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTACAAACCATCACTCGCATGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCATTAGCAGGCCGG
CAAGAACATGAGTGCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCAGAAGAGGT
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAACGCTCCTGGATGCCTAAAAAATAAGCAATG
TTAACAGTGAACTGTGCAATTAAAGCTGTATTCTGCCATTGCCATTGGCTTGAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GA~~TGGTTGACTCTT~~CACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAAGAGGAGCAGCTATGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCAGTGTAAAGATGCAAAAAAGATT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPD RDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYTIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACCGTGGCGGACCGTGGCGGCCACGGCAGCCCGGGCTGGGCAGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACATACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCGGGACAACCTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCACAAAGCAGCAGGAGGCCCCGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACGCCGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCTTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA
ATCGCGGCCACCACTGTAGGACCTCCCACCCACGCTGCCAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCCACCTGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKG
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPGPGTERPCGGYGCCEGEGRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCAGGGCA
GCACCATGCAGCCCCGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT
GCCCACCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGCTTCCAGG
AGCCGGTCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCGCGCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCCGTCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTCAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGGCACCTGCCGGAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTCTGGGCCTCGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGCATGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGGAGGGTACCAAGGAGAGCTG
GCGATGACTGAACGTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTTACTGCACATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTGTGCTGTCAC
TGGATCTGGCTAAAGTCCTCCACCACACTGGACCTAACAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPILLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPOLEHTLDLGDYGAQ
GDGDPPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTTGTCACTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGC GGAAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTTCCCCACCTCTGAATAACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCCT
TACACCCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTCTGGCTTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGGCCACTCTCTGTTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTCTGTTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGVMPNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAALVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGGGTTGGATGGCCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCACCCACCAAGTTCCAGTGCCGACCAGTGGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCACGGCCA
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCAGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCACTGCTGCGGTGC
TCAGTGAAGCCTGGTACCGCCACCCCTCCTCTTGTCTGGCTCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGACAAGCAACTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGCGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGCCACGTGGAACCTCGAACCCGAGCTCTGCAAGAATGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPCDSSDELCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCGCAGCGCGGGCAGCAGAGGTGCACAGATGCC
GTTAGACTGGGGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAAGATGTTATCATGGAATGAACCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCCGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGAAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAACGCTAACATCACTGTGATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTATTATGTCGCGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCCTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAATGGTAGTCACGGAGATTCGTCT
GCCACCCGGCCTTGTGAGCGTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGGCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTTAGGCCCGGGTACATGGCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGTGAGCTGCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCACCCCTGCTGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACCGCGTCCGCTCCCGGCCCTCCCCCCCCGCCCTCCCGTGCCTGGTCGGTGGCCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCCACGCCCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGGCGTGCTGCTGGTGGGCTGCCTGGCGACGGGTCGCCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAAACAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTTAGGAACCTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTTCATTGCAAATATTCTGATGAGAAACCAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAAGCTGCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTCTGTGGTACCAACAGGTCTGATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCAATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGCTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACGAAACTGACAACAATGGAAAAGAAATGATAAGAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTGGTTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTORPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVVCWVWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGTCTCCCTCAGGGCCGGGAGGCACAGCGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAACACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCATGGTGT
GTCAGCATGCGCTTGTGGACCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACACGGGCTCGGAGTCCTCTAAGCC
GCTCCCCTGGAGGAGCAGGTAGAGTGGAAACCCCCAGCTATTAGAGGTCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGACTTGTATCCAACCTACAAAGCTGGAGCCTGA
GGCAGAGAACAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTTTAATGACCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATTGAAACTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACCTGCTCTCAA
ACTCAGGTGATGGAAGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQUEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG
ACGGCTGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTAAAAACGCTGCAACAAGCATGCC
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTCTGGCCTTGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTACACTGGTGCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCAATTGTCTGTTCTGAAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGATAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQCOTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWECEDPFDLRLVG
GDNLCSGRLEVHKGVWGSVCDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGTCCGGACCGGTGGCGGACCGTGGCCGGTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTCTCCGGCTGCTGCAGTGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAACAGCTCATCAGAGA
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCACAGTGG
TGTGGACAAGAGGGTATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTCGTGCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGAGAAGCAGCACTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGTCACAAAGTGG
AAAGACTGAAGAACACATCTCGTCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAGGGCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAATTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAAEILQCFGYVDIL
VNNAGISYRGТИMDTTVDVKRMETNYFGPVALTKALLPSMIKRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVN
AITADGSRYGVMDTTT
AQGRSPVEVAQDVLA AVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNA
GTVTSDFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHSVPFL
LAYCSSKFAAVGFHKTLTDEAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEV
VNRLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACACGCGTCCGGACCGGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCGTGAGAGA**GATGGTTGGTGCCATGTGGAAGGTGATTG**
TTTCGCTGGCTCTGTTGATGCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATA
CAGAAGTGGTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCTCACCCCTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAAATTGAGTTGGTCGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATAACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTTTGGAACATGGGCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTCAGTAATTCAAGTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGGTAAGATCAACCTGAACCGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCGACTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACCGAACCTGAGGATCAGCTTACTATGAAATTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACGCATGGTTAAGTGAATAATTATAAGGTTCTGA
TCTACAATGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCATCAGGTAATTATTC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCAATTATGAAAAGGATGGATCCTTATGTTGAT**AA**ACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTGGGTCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGGTGAGCTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSILNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIIVAAALTERSLMGMDWKGSQEYKKAEKVKWKFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGGATGGCACATGTGGGAATCCCAGTCCTGTTGGCTACAAACAT
TTTCCCTTCTAACAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTCCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCCTAACATTGACTGGCTGGG
TGAACCTAACAGCCTTAACCTCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACAAAATAGATAACAGGATTCCCTAACATCCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCGAGTGGGACCTGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCCTCTGCCTGTGTTT
GCAGAACATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTGTGGCTCTCAGTGGCTGGGTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTTAACGACCTTCACTCTGAGAACATCGTACTGGACCTAACCAACTTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGTCTACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACGCCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCCGCTGGATGACCTCTCATCCTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCAACCAGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTACGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGTGG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTCGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCCTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTAGCTAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTGTG
ACTTAGCTTCTAGCTACTTCCCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTKNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKI PSDLALVSHFDIFYIYGFA SGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL AQA FNITSQDDVLFAIFSKGQKQYHHPPDD SALCAFPIRAINLQIKERLQSCYQGE GN
LELNWL LGKD VQCT KAPPV I DDNFCGLD IN QPLGGSTPVE GLT LYTT SRDRMTS VASYV YNG
YSVV FVGT KSGKL KKVRV YEFRC SNAIH LL SKES LLEG SYWW RFNY RQLY FLGE QR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGC GGACTGGAGTGGGAACCCGGGTCCCCCGCGCTTAGAGAACACGCCATGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGACTCCTGCTGCTGGCTCTGGGCTTCCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGGCTCCATCCACTATTTCCGTGTGCCCAAGGGAGTACT
GGAGGGACCGCCCTGCTGAAGATGAAGGCCTGTTGAACACCCCTACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGGCTTCCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGCAGTGAGATGGACCTGGGGCTTGCCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTATTGGACCC
TGATGTCCAGGGTGGTGCATCCAGTACAAGGGTGGGGACCTATCATGCCGTGCAAGGTGAGAAATGAATATG
GTTCCATAATAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC
TCCTGACTTCAGACAACAAAGGATGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCA
CAACACAGAGCTGCAGCTACTGACCACCTTCTTCAACGTCCAGGGAGTCAGCCCAAGATGGTGTGGAGT
ACTGGACGGGTGGTTGACTCGTGGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGACCAACTTTGGCTTCATGAATG
GAGCCATGCACTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGTCGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCCACCTG
ACCTTCTCCCAAGATGCCGTAGGCCCTAACGCCAGTCTGTACCTGTCCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCGAGG
TGTGGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACCTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTCGGCGTGGACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTGG
TAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAAGACGCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAGGTACGTTTGAGGAGACGATGGGGGCCCTGCATTACAGTTACGGAAACCCCCCCC
ACCTGGCAGGAACCAAGTACATTAGTGAGGGTGGCACCCCTCTGCTGGGCAGTGGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCCTCACGCTCAAAACCTAACGGCTGCAGGGAAAGGTGGGATGGCTCTGG
ACTGGGGCTACAGTCTGCCCTGTCTAGCTCAAGGGCTAACATCCCTCATGGCCCC
TGGCTTGTGATGGCTTCTACAGGGCTGCTCTTGCTGGGAGGCTGTGGGCTGTCTAGGGTGGGAGC
AGCTAATCAGATCGCTGGACTCAGGGTGTCTTGTGAGGAGGCTGTGGGAGGCTGTGGGAGGCTGTCTAGGGTGGGAGC
TGCAGGAGCATCTGCTGGACTCAGGGTGTCTTGTGAGGAGGAGGCTGTGGGAGGCTGTGGGAGGCTGTCTAGGGTGGGAGC
TTTATCCCCGAATCTGGGTGTGTCACAGGTGAGGGTGGGGAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCTTCAACACCTCTGAGCTTCTGGGATTCTGGAGGAACCTGGCGTGAAGAACATGTGACTTCCCTT
TCCCTCCCACTCGCTGCTCCCACAGGGTACAGGCTGGCTGGAGAACAGAAATCCCTCACCCCTGCCTTCC
CAAGTTAGCAGGTGTCTGGTGTCTAGTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGAGCAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCC
AGGGAGGAGGAGCAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGG
GGAGGAGCAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGGAGGAGG
ACAGAACAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCAACAGCAGGGCAGAGCAGGCCCTCCTTC
GAAGTGTGTCCAAGTCCGATTTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGCTCACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATACAA

FIGURE 64

MTTWSLRRR PART LGLLLL VV LGFL VL RRLD WST LVPL RL RHRQL GLQAK GWN FM LED ST FW
I FGGSI HYFR VP REYWR DR LL KM KAC GLN TLT YVPW NLHE PERG KF DF SG NLD LEAF VL MA
AE IGLW VILR PG PYIC SEM DLG GLP SWL LQDP GM RL RT TYKG FTE AVD LYFD HLM S RVV PLO
YKR GGPI I AV QVENEY GS YNK DPA YMP YVK AL ED RG IVE LLL TSDN KDG LSK GIV QGV LAT
IN LQSTH ELQ LLT FLF NVQ GT QPK MVME YWT GW FD SWGG PHN I LD S SEV LK TVSA IVD AGS
S IN LYMF HG GT NF GFM NGAM HFHD YK SDV TSY DYDA VL TEAG DYT AK YM KL RD FF GS IS GIP
L PPPP D L L PK MP YE PL TP VLY LSL WDALK YL GE PIK SE K P IN M EN LP VN GG NG QSF GY ILY E
TSITSS GIL SGH VHD RGQ VFV NT VSIG FLD YKTT KIA VPL I QGY TVL RIL VEN RGRV NY GEN
ID DQR KGL I GNL YLN D S PLK N FRI YSL DMK KS FF QRF GLD KWX SL PET PT L PAFF LG SLS IS
ST PC DT FL KLEG WE KVVF ING QNL GRY WNIG P QKT LYLP GP WL SSG IN QVIV FEET MAG PA
LQFTET PHL GRN QYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTACGGTCTGTCGCCGTCTCAGACTAGAGGAGCCTGAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTCGTCCCTGCTGCGCTCAGCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGCC
CGTCCGCTATGTGTCGGCAGCCTGCACTACTTCGGTACCGCGGGTGTGCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCTAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCATCCTGGTGTGCTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTCCTGCCGAGTGGACTCCTGGTCAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT
CGGAAGTATGAACCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTAGCTGTAACCAAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCGATAAGAAGGGACGCTTCCTCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTGCTCTCGAGATGTACAGCAAGT
TCCAGGAAGTTCCTTGGGACCTTACCTCCCCGAGCCCCAACAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGTGCTTGGCCCCGTGGGCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTTATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAACATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCAAACCTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAACCTAACGGCCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTAACCGAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAACGCTCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTTGAAAGGTAGGCCGGCATGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGA
SVNM
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVP
LGPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTH
TIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNM
RDKLFLTGKLGSKLDILVENM
GRLSFGNS
SSDFK
GLLKP
PILGQTILTQWMMFPLKIDNLV
KWWFPLQLPKWP
YQAPSGPTFYSKT
FP
I
LGSVGDTFLYL
PGWT
KGQV
WINGFNL
GRYWT
KQGP
QQTL
YV
PRF
LLF
PRG
ALNK
ITL
LE
EDV
PL
QP
QV
QFLD
KP
I
L
N
S
T
S
T
L
H
R
T
H
I
N
S
L
A
D
T
L
S
A
E
P
M
E
L
S
G
H

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCCTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATCCAGATGTCAAAACGATT
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCCAGTGCTGCTTGCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTAAAAA
CCTTCGAGAGAGTTGTACTTAATAGGCAATTGAACACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTTCTCTAACACAAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATACCCTGCCACTCGAAGTCAGGAAAGAGGATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTAAAGTCATTCAATTCCAAATCATTGTTTTAAATTGTTGTA
AAAGGAAAGGAAAATTATAACTAAATCTGAGGACTTGAATGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPA WYVYLLK NLRELYLIGNLN SENNK MIGLES LREL RHL KILHVKS NLTK VPSN
ITDVAPHLT KLV HNDGT KLL VLNS LKK MMN VAE LE LQ NCE LERI P HAIF SLS NLQ E LD LKS
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTI PPS ITHVKNLES LYFSNNKLES L P VAV FSL Q
KLRCL DVSYNN ISM IPI EIG LLQ NLQ HLH ITGNKVDILPKQLFKC I KLRT LNL GQ NCITS LP
EKVGQLSQLTQLELKGNCLDR LPA QLG QCRMLKKSG LVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCTCGGCCCTCTCTGGACTTGCAATTCCATTCCATTGACAAACTGACTTTTTTATTCT
TTTTTCCATCTCTGGGCCAGCTGGGACCTAGGCCGCCCCGGAAAGACATTGTGTTTACACATAAGGAT
CTGTGTTGGGGTTCTCCTCCCCTGACATTGGCATTGCTTAGGTAATCGAAGTCTTGACCTCATACTGATTATGCCTGTC
GCTCAGTGCTTGCTGCACTATCTGCTTAGGTAATCGAAGTCTTGACCTCATACTGATTATGCCTGTC
ATCGCTGGTGGTACCTGGCCCTTGCTCTGCTGATAGTGTGCTGCTGTCTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAAATCACAAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACCATGCCACGGAGCTTGCTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTG
AGTTTGATTCCCTGCCACCTTGCTGCGACATAATGAGGGCCTTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCTGCTGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCCAGGAAGGAGTTGGGAGAGAGAACCCACTGTGGGAATGCTGATAAACCCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCTTAAAGGCTGCCAGGCCCTGCCAAAATGGAGCTGTA
AGAAGGCTCATGCCATTGACCCCTTTAATTCTCTCTGTTGGCGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTCCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAAGTGAACATTAAAGCTTGTGACGGAACCTCCAGCAATGGCCTGCTGAGGG
CAAGTCTGCACTAAAAGCACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAECTCAGCAAGAAATTCAAAGAACTGTCTTGTCTACTACTTCTCTCCTAACATCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGAAGGATCCTCACAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTCAAATTGATTCTTGCCATCTATGATGGCCCTCCACCAACTCTGCTGATGGACAAGCTGT
GGCGTGTGACTCCCACCTCGAACATGTCATCAAACCTCTGACTGCTGCTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTCTGCTTCTAACACCTCAATTATGCAAGAAAACATCAACACTACATTAACTTAACTGCTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAACATGGAATAACTTGCAACTAAA
GACCCAACITGCAAGACAAAATTATCAAATGTTGGAATTTCCTGCTCTTAAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCACTCTAACATTCTGAACTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGCAAATATAACACCAAGCATGGCTTTTGAAATCCAATTCA
TTGAAAAGACTATACTTGAAATCACCATATTATGTTGAAACCAACTCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCAAATTGGGGTGTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAAATGCCCTTAAATTCTGAGAAGTATGAGCTCTGTGATCTGAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCAAGTCTCGCTGCAATCAAGGTTGTCTCCAGAAGCAAACGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCACAGTGCACATTCAAGGATTTCAGCAT
GAAACACATGCGGAAGAAACTCAAACCCAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTCTG
AATGTGGTGAATGCGACAATCACAGTGAGGCATTGAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCAAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCCTGCATGTAACAAAAAA

FIGURE 70

MELVRRRLMPLTLLILSCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLNPE NCTWTI
ER PENKSIRIIIFS YVQLDPDGSC ESEN IKVFDGTSSNGPLL GQVC SKNDYVPVFESSS STLT
FQIVTDSARIQRTVFV FYYFFSPNISIPNCGGYLDTLEG SFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQS QNALGKYNTSMALFESNSFEKTI LESPYV DLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGC VSRSKRD ISSYKWKTDSIIGPIRLK RD RSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCCGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCAGGAGCTCCCCAGGCTCGCTTGTGCTGTTGCTGTC
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCAGCTGCTGACCCCACCTGGAGTCC
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAGTTCGCATCTCATCCACTG
GGGAGTGTGCCCCAGCTCGTAGCGAGTGGTCTGGTGGATTGGAAAAGGAA
AGATACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTAGTTCAAAATATGAAGAT
TTTGGACCACTATTTACGAAAATTTTAATGCCAACAGTGGCAGATAATTTCAGGC
CTCTGGTGCCTAACATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGT
CAGAATATTCTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCCTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTCTCCTTGAGGATGAATCCAGTTCACTCCATAAGCGGAATTCCAG
TTTCTAACAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTCTGGCTGGTT
ATATAATGAAAGCCCAGTTCGGGCAAGTAGTCACTGTTACCTGAGGACATCTTGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCACTGATCGTTATAACCCAGGACATCTTGTCCA
CATAAATGGAAAAGTGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCATGCCATTCTTAAATGGGCCACATCAGGACAGCTGTTCTGGCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAATGGCATTATGGTAGAAGTGCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACCTGGATAAGAAAATTATTGGCAGTTCAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTACTCAGAGGTGAGAATTCTTACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAAGTGAACAAATTATGGTAGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTGTGCCAACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAATGGTGCACCTGTATAGGGCACTTACACAGAATGGAG
CTTACAGGACTGGAAAGTGTCTGGGTGAGTCAGTGAATGTGAAGGCCAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCATTAAACATAAGTGTACTGTAACATTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPPSFKYEDGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSCTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGWSLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNW
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACG**A**TGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCTGGCCAAGGCTCTTGCAGCAGAAGAGCT
TTCCATCCAGGTGTAGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCAGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTTAGGATTAGCCCCAACCCCAAGTGTGGAAAAATGGGTTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCACCAAAGATCCCATAATTCAACACTCA
AACTGCAACACAAACACAGAATTATTGTCAAGTGACAGTACCTACTCGTGGCATCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTACAAACAAGAATCAGCAGAAGGAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGAACACTACCGTGCATGCCGGAA
GCTGAAGTT**A**GATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCAAGCTGGGAATCAAAGGGCCAAGAACCAAAGAAGAAAGTCCACCCCTT
GGTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCTACCTCCAAGCTTCCCACGGCC
TTCTAGCCTGGCTATGTCTTAATAATATCCCACCTGGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGCTTCTGAGGCCGGTA
AGAGCAAAGAATGGCAGAAAAGTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGAAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTACAAAATAAAACTCTTATAAATTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCTAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTCA
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTTTATTTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGGCCATTACAAATGTATCACTA
GCCCTCCTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTGTCACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLAEAV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGC~~CC~~GACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGCCCTGCTCTGCTGCCTTCACTCGTGAGGAA
ACTGCCGCCCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAAAAGATCCTCATTGGCAGTGCTCCTCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTCTGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAACGTAAGATGCTGGGTATAGAA
CGCTAACGAAATTTCACCCCAAGGACTCTGCTCCTAACGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACCTGTCGCTAGTCCTAACGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCTATTTGTGGGATTGAGAACGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAACCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEEELERDKRVTWIVEEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFKGVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

FIGURE 78

MGLLLLVPLLLPGSYGLPFYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVEELRGVVFPYQSPNNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGYPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**GATGAT**GTGGCACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGCCAGGGAAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGC~~GG~~CCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACC~~GC~~CGCGGGGAC
GGCGACGGCTGGGTGCGCTGGCGAGCTTCGCGGTGGATCGGCACACGCAGCAGCGCA
CATACGGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCGCCGGTGAAGAATTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACAGCGCGTTCGGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCGCACCCCGAGG
AGTCCCTCACATGCCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGGAGGTGGCCACTGGTGCTGCCCTGCCAGGACAGCCC
CTGGTGAAGCCAACCACCTGCTGCACGGAGAGGCACACGGACAAGGATGGCGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAG**GTGAG**GCACCGCGCAC~~T~~GCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGCCGCTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTGCGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPISDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDRDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEYIADLYSAEPGEEPAWVQTERQQ
FRDFRDLNKGHDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTCGCTCCCAG
CCTGTCGTCGCTTGGCGCCCCCGCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCGCCGAGGGCCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGTCCTCTCCTCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGCGGGCCTCCGCACCTGGCCTGCCGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTACCAATGTCCGCAAGCCTGGATCCCGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACCAAGGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTATGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAAACAGGGACTAACAGGACTAAAGAAAACACCCGAGAAGAAA
GTGTCCACAGCACATCCACCAACAGGTAAACAGACTAAAGAAAACACCCGAGAAGAAA
CAATAAGATTGTAAGCAGACATTGCATTTCTGATTGATGGAAGCTTAAATTGGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGGCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTGAA
AAACTTACATCAGCAAAGATGTTTGTGCAAGGGAGTAGGTTCAAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCAAAGTGGTGGTATTATTGATGGTTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACACATGCCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGCAAGAACCTGTTATAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTCCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTGTATT
CTCATAATACTGAAATGCTTCTGACATACTAGAACATCAGATACAAA
ACTTGTGTTAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAACATTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCTCCGCACCCGGCCCGCCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCAGGCTCCGGCGGGAGCGAGCAGATCCAGTCGGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAG**ATG**CAGCGGCTGGGCCACCCCTGCTGCCTGC
TGCTGGCGGGCGGCTCCACGGCCCCCGCGCTCGACGGCGACCTCGGCTCCAGTC
AAGCCGGCCCGCTCTCAGCTACCCGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGACCTGATG
GAGCCTGGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGAGCGTGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTTCATGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGGCTGCCGGCT
GCACTGCTGGAGGGGAAGAGATT**TAG**ATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCAGGTGTGCTTGTGCTTGTGCTGACCAAGGCTTCTTCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCACT
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTGGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAAGTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGTGAAACACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT
CTGGTTGTGACTCTAACGCTAGTGTCTCTCCACTACCCACACCCAGCCTGGTGCCACCAA
AAAGTGCCTCCAAAAGGAAGGAGAATGGGATTTCCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACTAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACTGAGGTTAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCATCCACTCTCCCTCCCAAACACACATGTGCATGTACACACACATACA
CACACATACACCTTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGCACAGGCCATTACCTCTGCAGCTCTTGCTTGAGTCAGAAAACATGGGAGGG
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCACTGAGGTCAAGGAG
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTACTAAAAAATACAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCAGGAGAATCGCTGAACTCCAGGAGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACACAGGGAGGA
GGGGTAGATACTGCTCTGCAACCTCTTAACTCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGGCAAGAAGTGA
GCCCCCGGTGAGCTGGGAGGGGGTCTGGGCCCCCTGGCAGGGTTGCTGACCCCTACCCCTGCAAACACACA
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGAGCTCCACCATGAGGCTCTCGTGGCCCC
ACTCTTGTAGCTGGGTGGCTGGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTGCCTGCCAGATCGGCCCTGGTATACGCCCGCTGCTTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACCTCCCGCAGGCACACAGACCCCTGCTCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACCACAGCTTGTGAGGGCTGCCAGCCTACAGGAACCTATCTCAACCACAAACCAGCTACCGC
CCCCAGGGCTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCAATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCC
GAACACTCCGGCCCTGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACTGCGGGAGATCTCCGACTATGC
CCTGGAGGGCTGCAAAGCTGGAGAGCCTCTCTATGACAACCAACAGCTGGCCGGGTGCCCAGGGGGCACT
GGAACAGGTGCCGGGCTCAAGTCCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGC
CAACATGCTGCACTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCATGACAAGTTGCC
GAACCTCCCGAGCTGACCAAGCTGGACATCACAATAACCCACGGCTGTCTCATCCACCCCCGGCCTTCCA
CCACCTGCCCTGGAGGACCCCTATGCTCAACAACACAGCTCTCAGGCCCTTGACCCAGCAGACGGTGGAGTC
CCTGCCCAACCTGAGGAGGAGTAGGTCTCCACGGCAACCCATCCGCTGTGACTGTGTCATCCG
CACGGGCAACCGTGTCCGCTCATCGAGCGCAATCCACCCCTGTGCTGCGGAGCCTCCAGGCC
GGTCCGTGAGGTGCCCTCCGGAGATGACGGGACACTGTTGCCCTCATCTCCCCACGAAGCT
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGATTGCCGGCACTGCCGAACCCGAACCGAGATCTACTG
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAAGGAGGTACCGGGTGTACCCGAGGGACCC
GGAGCTGCGGAGGGTAGCAGCAGAAGAGGCAAGGGCTATAACACCTGTGTTGGCCAGAACCTGGTGGGG
TAAGACGGTTAGTGTGGTGTGGCCGTGCTCTCCAGCCAGGCAGGGAGCAAGGACAGGGCTGGAGCTCCG
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTCAACCCACCCACAGTGTCC
CACACAGCTCA
CTGGTCCAGTGCCCTCCCTCCGGGGCCAGGGGGCACAGCTCTGGCCCGCTGCCTCGGGAAACCCACAGCTA
CAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCTGCCGTCAAGTGGCTTGTGATGCC
GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTTCTGCCACAGGCCATTAGGGATGTC
TGCCATCCTGGCTCTGCTGCTTCTGCCAGCTGGCTAGCGGGCACCTGGCACAGGCC
GGGTGTGGTGGGAGGGGGCTCTCCAGCTGGCTTCTGGGCTGGAGTGC
GTCTGCTCCCCCTGCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAATTCTGAGCTCAGGCCCTGCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGGCAGGAAAGGGACATGGACCCACGTGCTGAGGGCTGGCAGCTGGC
CAAGACAGATGGGGCTTTGTGGCCCTGGGGTCTGCTCTGCAGGCCCTGAAAAAGTTGCCCTTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGGAGGACTTGGCTAGAGCCTCTGCC
CTCTCTGCCAGGGCTCTGGCTTGGCTTGGCTACCTGTGCTGGGGCTGCACCCCTTCTCTTC
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGGCAAGGGCTGAAGGAGGCCACTCC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCAAGCTGACTTTCTATAGGCAATTGTAC
ATGTGTACACTCCCCAACCGATTCACTTTCTCTGTTGTAAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATAATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTLDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLAGMNLRREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMELTMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPPEIYWVTPAGLRLTPAHAGRYYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVALLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGGCCACACTCTCAAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTCTACGGCTCATCTGCATGTA
CACACTGTGGTGATGCTACGGCGTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCCTCATGCTGCACCTCATGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGCTTCTCGAGGTGAGTGAAGAACAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACCGTACCCATCCCC
CAGCATTGCCAGCTCACGGGCCTCAAGGAGCTGGCTCTACACAGCGGCCAAGATTGAAGCGCTGCGCT
GGCCTTCCTGCGCAGAACCTGCGGGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGGGAGAACAAACCGCTACATGTCATCGA
CGGGCTGCCGGAGCTAAACGCCCTCAAGGTGCTGCCCTCAAGAGCAACCTAACGAAGCTGCCACAGGTGGTCAC
AGATGTGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGGAGCTGGAGCGATCCCCCACCTCCATCTCAGCCT
CCACAAACCTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
GCACCGCCTCACCTGCCCTAACGCTGTGGTACAACCACATGCCCTACATCCCCATCCAGATCGCAACCTCACCAA
CCTGGAGCGCCTTACCTGAACCGAACAGATCGAGAAGATCCCCACCCAGCTCTTACTGCCAGCTGCG
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCCCTGCCGACATCGGCCCTCTGCGAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGCCTGAAGCTGCCAGCTGCC
GGGCAACAAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCC
CAACCCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCCAGTGCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGGAGGGCAGGCCAGCTGCTTCTCC
AACTCCGGACAGCCAGGACAGCCTGCCGGCTGGCAGGAGCCTGGCGCTTGTGAGTCAGGCCAGAGCAGA
GGACAGTATCTGTGGGCTGCCCTTCTCCCTCTGAGACTCACGCCCCCAGGGCAAGTGTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGCTCTCCCTGGAGGCCAGCTCTGCCAGGGCTGAG
CTGCCACAGAGGTCTGGGCCCTCACTTTAGTTCTGGTATTATTATTTCTCATCTCCACCTCCTTCATCC
AGATAACTTATACTACATCCTCAAGAAAGTTGAGCCAGATGGAAGGTGTTGAGGGAAAGGTGGCTGCC
TTGTCCTTATTAGCGATGCCCGGGCATTTAACACCCACCTGGACTCAGCAGTGGTCCGGGGCAACCA
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGGCTCTGCCGCTGGCTCCACGGAGAGCAGGCC
AAGGCCAGGCCCTGGAGCTTGCTCTCAGTTTGTGGCAGTTAGTTTTGGTTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGAAAATGGATGGTTGGTATTAAAAAGAAAAAAACTTAAAAAAA
AAAAGACACTAACGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAG
TGAACGTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGGAGGGAGGTTTTGGTTGGTTGGTCTTGTGTTCTTCTCC
ATGTGTCTGGCAGGCACTCATTTCTGTGGCTGCGGCCAGGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGGCTAATCCCCGATGAAACGGTGCCTCATTGCACCTCCCTCGCCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGGCCACTCGCCCAGACTTGTCTTCCCCACCTCCTGCCATGGGTGT
CCAGTGCCACCGCTGCCCTCCGCTGCTTCCATCAGCCCTGCGCCACCTGGCTCTCATGAAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTCGCCCTGGAGGGCAGGCCAGGGCTGGTCCAGGCC
CTGGAGTGCACACAGCCAGTGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTCGGGTCCCCACCT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAACGGCACGTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCGTCCATTGTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGACACTAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGCTGAACTTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFVDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDRQRLTKNAQDKLELHLFMLSGLPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSQLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVQLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGCAGGGACCATCAAGTGCACACTTGCGGGG
TGCCTGGGTGATTCTGGATCTCCCTGGATTCTCGCTCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTGTCTTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACATGGGTCAAGGAGGC
GGTGGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCC
ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAETCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCCTGCTTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNLTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCAACCTGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATAAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCACCTGTACACTAAACACATCCAGCCCCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCACATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTAAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSSLHRWALTAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCCGTGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCCTCAATAACGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGGCCATCCC
CACTGACCCCTCCACACGGTGAAAAATGGCTCTGGCAGCCGGAGCCCAGAAGTGCACATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCGATAACAACCTTGACCTACAAGACGTGG
GCTCTGGCACCGAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTCGGTGGCAACCTTGACATCAGGCATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCCCTGCTCTGCCCTCAGGTGACAGT
GGGGCCGGGTGGTGGTCTGTCTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCAG
CCCCTATGTACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATTCACTTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGGGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTGGCTTCTCAACCCAAAG
GCTCTACCAGCAGCATGGGCAGGTCTCTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTGTGAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTTCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTTCAATCAGGCTTCTCAAAGGGTTGTATACAGACTCTGTGCACTA
TTCACTTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAAATGCCCTCCAGTGCATACTCTCAATCTTGCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCCTACTTAGCTCCAGGTCTTAACCTCTCTG
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGAGATTTGCTCTCAGTTACTCATTGCTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTEHVVRSPHPYQLPQALAPHVDFVGGHLRFPPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFNSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGCCCCACACCTGTCAGCGCGCAGCGAGCCGGCCGGGC
GGGCTGCTGGCGCGAACAGTGCTGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTAACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATAACCGCCTCCCTGTCGTCTGCCCAAGTCTACCCCTAACCTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTACAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGCCATGCCAGCAGATGAA
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTACAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGGCAGAACATTCACTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGTGGGAGCGAAAAATTATTGGCATTTTCAGG
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTGTCTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTGTGTGTGTGTGT
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
AAHCIHDGKTYVK
TQKLRVGFLKPKFKDGGRGANDSTS
AMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKH
RKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYD
LLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCTGGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGTGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGTGTTGCCCTGGTGGAGC
CCCACCCCTGTGTATT CCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCTGGGTGGAGAACGATCGTGAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCG
CCGGCGCTCTAGGGCGCAGCGGGACGGGGCTGGATCTGAAAGGCGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGGCGTTCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATT TAT
AGGTATTTGTAACCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCAACGACAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCATCCCCAAATCAGCAGACAAAGTGAACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCGCAGTCGCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGATCTTCTTGAATGGGATACCACTCAAAGGG
TGAAGAGGTCA GCTGTCCTCCTGTCATCTTCCCCACCCCTGCCCCAGCCCTAAACAAAGATA
CTTCTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGGTGGCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATT CCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAA

FIGURE 100

MHGCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLRYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGI PAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSILAHSPLSLDEEPVTFPKS
THVPIPKSADKVTDKTVPSPRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTAGGCTTCAATTGGAGCCCCCTAACAGAACCGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCGCTTGCCTTACATTAGCAGACCGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAGTGAACAAACATGAATTGGAGACCATTC
AAATCTGGGACCAGTCGCAAATATTACACTCTCTCCCTGGCTGAAACAGGATTGTTGAAACTCCCTGA
ACATCTGAAAGAGTTCAGCCCTGAAACTTGGACCTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGATCTAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGGCCAACACAACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAAACCGAAACAAGATTAAGATGGACTGACATTCCAAGGCTTGG
TGCTCTGAAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGCTTTGGGGCTGAGCAA
CATGGAATTTGAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGATGCT
GCAGGAACTTCATCTCAGCCAAATGCGATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTCAATCACTTCAAGGTTAGATGATTCAAGCTTCCCTGGCTAAGCTTAACTAAC
ACTGCACATTGGAAACACAGACTGAGCTACATTGCTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGCTTTACAAGGCAATGCATTTCACAAATGAAGAAAATGCAACAATT
GCATTAAATACATCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACCT
TCAGAGTTGTAATGCCAGTTGTGCCATCCTCAGCTGCTAAAAGGAAGAAGCATTGGCTGTTAGCCCAGA
TGGCTTGTGAGTGTGATGATTTCCAAACCCCCAGATCACGGTTAGCCAGAAACACAGTCGCAATAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCAGTGATCCCCATGACTTTGCTTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGGCAGGGTGTGGAGTATACCAC
CATCCTCGGCTGCGGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACC
CCGAGCTGGGGCATGGCACGCTTGGAGTGCTGCTGTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGATGTGATGCCAGGGTGTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGAGGAAGTATTCAGCAAATGC
AACTCTGACTGCTCTAGAACACCATCATTTTGGGCCACTGTTGGACCGAACGTGTAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTGGGTT
AACCGAGAGGCACTTTTCAGCAGGCAATCAGCTCTGATTATTGAGCTCAGATGTCAGTGTGATGGGAA
ATACACATGTGAGATGCTAACACCCCTGGCAGAGAGGAAACCTGGCCCTCAGTGTGATCCCCACTCCAAC
CTGCCACTCCCCATGAGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTTGGGTGCTGATCATAGC
CGTGGTTGCTGTGTTGGCACGTCACTCGTGTGGGTGTCATCATATACACACAAGGGGAGGAATGAAGA
TTGAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGTAGTGTCTTCAGAAAGTGGAGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC
CACAGATCTGTTCTTGCCGTTGGGATCCACAGGCCCTATGTTGAGGGAAATGTGATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCACTGCCAGCAAGAACAGTTTAATGGACCAACTATGAGCCAGTT
CATAAAGAAAAGGAGTGTACCCATGTTCTCATCCTTCAGAAGAACCTGCGAACGGAGCTCAGTAATATATC
GTGCCCTTCACATGTGAGGAAGCTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTAACTGAAATCCAGAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGGTAGAGGAAGATGGGAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGACCTTAAACAGACTTTAGAAAACAGACTCCAAATTTCAGTC
TTATGACTGGACACATGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTATT
AAAGAGAGAAATCTTATGTTTAAATGGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGAT
GAACCAAATACAAAAAGTTATGAAAATTCTTATGAGCTCAGTGTGTCATATAAGAACATCTTAAACTA
TTTTTAACCTTGTGTTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGTACCAATT
TTAAATAGAAGTTACTCATTATATTGACATTATTTAATAAAATGTGTCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSPFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEIILQDHNNLTEITKGWLGYGMLQELHLSQNAINRISPDAWE
FCQKLSELDLTNFNHLRSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLIDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQQLHLNTSSLLCDCQCLKWLPQWVAENNQSFVNASCACHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYCTAQN
SAGSIISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPQKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRSLVIPTPTCDSPQMTAPSLODDG
WATGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIAD
RQDGYSSESQSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSFNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTCAGAAAGA
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAGTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACAGAGTTAGACCCGGGGGTGGTGTCTGACATAAATAATCTAAAGCAGCTGTCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATCACAAGAAAAAGTAGTTCAAGAATGAAA
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAGTTGGGGCTTTTAGTAAAGTAAGAAACT
GGTGTGGTGGTGTCTTCTTGAATTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCCAGATTGAGGCATTGATTTGGGGAGAGAACAGCAGAGCACAGTGG
TTTGTGCCATGTGACTAAATTGACGGATAATTGCAAGTGGATTTCATCAACCTCTTTTTAAAT
TTTATTCCTTGGTATCAAGATCATGCGTTCTCTGTTCTAACACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAATGTTGAATTCCAGAACCCAGATAAAATTATGAATGTGAAACAAGAT
GACCTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGGCCATTGACCCCTGCTGTGGTCT
GCTGGCTCTTCAACTCTGGTGGCTGGTCTGGTGGCTCAGACCTGCCCTCTGTGCTCCTGCAGCAA
CCAGTTCAAGGTGATTGTGTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCCTCAAGCAGCTGAGGACTTGGAAATCCT
ACAGTGAGTAGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA
ACTTTGACAATCGTCTTACTACCATCCGAATTGGAGCTTGTATACTGTCTAAACTGAAGGAGCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTTATGCTTTAACAGAACTCCTTGCAGGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATTTCTGGAAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGGCAGAT
TCAAGTGAACGGAAATGCCCTTGAACACCTCAGTCAGTGGAGATCAACCTGGCACACAATACTAAC
ATTACTGCCTCATGACCTCTCACTCCCTGACATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCCTGTTGTGCCCGGTG
TAACACTCCCTCCATCTAAAGGGAGGTACATTGGAGAGCTGACCCAGAAATTACTCACATGCTATGCTCCGGT
GATTGGAGCCCTGACACCTCAATGTCAGTGAGGATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGATCTGGATTACTCCAATGGAACAGTCAGTGCACACATGGGGCTACAAAGTGCAGTAGCTGT
GCTCAGTGATGGTACGTTAAATTCAAAATGTAACCTGTGCAAGATAAGGATGTCAGTACATGTTGAGTAA
TTCCGGTGGGAAACTACTGTCTCAGGCCACCCCTGAATGTTACTGTCAGCAACCAACTACTCCTTCTTACTTTC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACCGAACAGATAACAAATGTTGGTCCCACCTC
AGTGGTCAGTGGAGACCACCAATGTCAGGACCTCTCAGGATGAGGACCGAACAGATAACAAATGTTGGTCCCACCTC
CACCACCCAGTGAATGATATAAACAGTGGGATCCAGGAATTGATGAGGATGAGACTACAAATCATCAT
TGGGTGTTGTGGCATCACACTCATGGCTGAGTGTGTCAGTGCAGTGCAGTGGTCAAGATGAGGAAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAGGACTGTGAAATTATTAAATGTTGAGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAACTATAACTCATACAAATCTCCCTT
CAACCCACACAACAGTTAACACAATAATTCAATACACAGTTCAGTGCAGTGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAACAAACATCAAAAAAA
GACAGTTATTAAAGACACAAATGACTGGGCTAAATCTACTGTTCAAAAGTGTCTTACAAAAACAA
AAAAGAAAAGAAATTATTAAAGTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCIDIL
WLSWWIKDMASTSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWEETNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCA GTT CCGTT TCCCTCGCTGTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACC CGGGCAGCGCAGGGAGGAGCGCGCACCGCACCG
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTGTCGCCGGGCCCCGAGCGCGCGCGCGCTGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCCCGATGAGCGGCCGAGCCTCCGTGCGCGCCGCGGGGTTGGGCTGCTGTGCG
GCGGTGCTGGGCCGCTGGCCGAGCAGCGCCGCTGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCAGTCGTAAGGGCTAGCGCTCTT
CCGAGCCACTCCGCTGGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
ATGAGCACCTCAAAGCCTTCGAGAAGTGAAGACTGAACAACAATGAATTGGAGACCATTCAAATCTGGGACCA
GTCTGGCAAATATTACACTCTCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCAAACGTCATTTCCAGGCCACAG
CTCAAATATCTGTATCTAACAGCAACGAGTCACATCAATGGAACTGGTATTGACAATTGGCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACGAATCTAGCTATCCCACCCAAAGATGTTAAACTGCCCAACTGCAA
CATCTGAATTGAACCGAAACAAGATTTAAATGTAGATGGACTGACATTCAAGGCCCTGGTGTCTGAACT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAAATTG
CAGCTGGACCATAACAACTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGCTGAGCTGGACCT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTACAAGTTAGATGATTCAAGCTTCTGGCTAAGCTTAAACTACACTGCACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGCTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGCTTGACAAACTGAGGGCAGTGTACTC
CAAGGAAATCGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGGAAACAAACTTTCAGAGCTTGTA
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTTTGCTGTTAGCCAGATGGCTTGTGCTG
GATGATTTCACCAACCCCCAGATCACGGTTCAGGCCAGAAACACAGTCGGCAATAAAGGTTCCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTTGGAAAAAAAGACAATGAACTACTGCATGAT
GCTGAAATGGAAAATTATGCAACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAACATCCTTCGGCTG
CGCGAGGTGAAATTGCGCACTGAGGGAAATATCAGTGTGTCATCTCCAATCATTGGTTCATCCTACTCTGTC
AAAGGAAAGCTACAGTAAATATGCTCCCTCATTCACCAAGACCCCCATGGATCTCACCACCGAGCTGGGCC
ATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGACCCCCCAGATAGCCTGGCAGAGGATGGGGCACAGAC
TTCCAGCTGACGGAGAGACGCATGCATGTGATGCCAGGATGACGTGTTTATGTGGATGTGAAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGCCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACGGACAAAGATGATAGCCATTGGTGTAAACGGAGAGGCC
TTTTTGACGAGGAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTCGCGCCCTAGTGTGATCCCCACTCCAACCTGCGACTCCC
CAGATGACAGCCCCATCGTAGACGATGACGGATGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTG
GTGGGGCACGTCACTCGTGTGGTGTATCATATACCAACACAAGGCGGAGGAATGAAGATTGCAAGCATTACC
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTGATCTCAGGGACGTTAGCTGACAGGCAG
GATGGGTACGTTGCTTCAGAAAGTGGAGGCCACCAAGTTGTCACATCTTCAGGTGCTGGATTTCCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAAGCTGATGTGAGCTGCCACAGATCTGTT
CTTTGTCGTTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGTAATGGCTCAGATCTTTGAAACA
TATCATAACAGGTTGCACTCCTGACCCAAAGAACAGTTTAATGGACCACTATGAGGCCAGTTACATAAAGAAAAG
GAGTGTACCCATGTTCTCATCCCTCAGAAGAACGGAGCTTCAGTAATATATCTGTGGCCCTTCACAT
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAAATCTGTCATAAACAGTCC
TCTTAGTTTAGTGCACATCCAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGGTACCTTGGAAA
GCTCTCAGGAGACCTCACCTAGATGCTTCAAGCTTGGACGCCATCAGATTGTCAGGCCAGAGCCTTTAT
TTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAAGAGGAAGATGGGAAAGAACAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAATTTCAGTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACACTACCTCAAGTGAACTTTATTAAAGAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAGTTATGAAATTAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTATTGTTAAACTATTGTTAACTT
TTTATGCAAAAAGTATCTACGTTAAATTAATGATATAATCATGATTATTGTTATGTTATGTTATAATGCCAGA
TTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGTT
ACTTCATTATATTGACATTATTTAATAAAATGTGTCATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAAPERCPPTCRLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASIPPKMFKLQPQHLELRNPKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWEFC
QKLSLEDLTFNHLRSRLLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQHLNTSSLLCDCQLKWLQPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFCDDF
PKPKQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVDSDVSDAGKYCEMSNTLGERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHSEESCRSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYLDLT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCCAGCTTGAATGAAAGGAGCCCGAGCCGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTCGGCCTGTGGGCGCCGTCGGCGCCGGCGCAGCAGGGAAAGGGAAAGCTGTGGCTGCC
CTGCTCCACGAGCGCCACTGGTGTGAACCAGGGAGAGCCCTGGTGGTCCCGTCCCCTATCCCTCCTTATATA
GAAACCTTCCACACTGGGAAGGCAGGGCAGGGCAGGGCTCATGGTGAAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTCCGAGTTACAGATTTCAGATAACCAAATGGAAGGCCAGGAGGCAGAACAGCCTGCCGTGGT
TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGGCCGGGTGCTGC
TGCTCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGCCCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGGCCGAAGAGAACGAATTGGGAGGGAGGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGCTGCCCAGCCGGTCACTGCCCCGGAGACTGTGCTTGCCTGAGGAGGCCGGTGTGGACTGTG
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAAGAACACCAGC
TGGAAAAGATCTACCTCTGAGGAGCTCTCCCGCTGCACCGCCTGGAGACACTGAACACTGCAAACAAACCAGC
CTTCCCAGGGCTCCAGAGAAGGCTTGAACATCTGACCAACCTCAATTACCTGACTTGGCAATAACAAGC
TGACCTTGGCACCCCTTCTGCAAACGCCGTATCAGTGTGGACTTGTCTGCCACTATCTACCAAGATCT
ATGGGCTCACCTTGGCCAAGGCAAACCTGAGGTCTGTGTACCTGACAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCAGGTCTCATCTGTCAGCAACTTCCCTGCGCACGTGC
CCAAGCACCTGCCCTGCCCTGTACAAGCTGACACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGAGCTGAGCAGCCTGCGAGCTATACTGCAAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCCTGGGTCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAACGCCATCCGGAGCGTGGACGCAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTTGCACACGGTGACCTGTACAACAACAGCGCTGGAGCGCGTGCCAGTGGCCTGCCGTGTC
GCACCCCTCATGATCCTGCACAACCAGATCACAGCATTGGCGCAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGTGCACCGCAGCCTCGCAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTCGGGCAACCGGCTGCACACGCTGCCACCTGGGTGCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCGTGCCTGGGTGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACCTGGAGTACCTGTACCTGCAAGAACACA
AGATTAGTGCCTGGCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAGC
TGGCTGTGGCTCCGCTGGACAGTGCCTCCGGAGGCTGAAGGCACCTGCAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTACATTTCAAGGACCGTGGCCCTTGGGAAGGAAAGGAGGAGGAGGAGGAAGGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTCTGC
AGCACACGCCCTGTGCTGTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCACGGCCAGACACATGC
ACACACATCACACCCCTCAACACCCAGCTCAGCCACACACAACCTACCCCTCAAACCCACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAAGGGCTGCCCTGCCACACACAGGCCACCA
TTCCCTCCCCCTGCTGACATGTGATGCTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTTGTCCCCAGCCAGAATCAGCCATAGCAGCTGCCGTGCCCT
GTCCATCTGTCCTGCCCTGGAGAAGACACAAGGTATCCATGCTGTGCCAGGTGCCCTGCCACCCCTCT
GGAACTCACAAAAGCTGGTTTATTCTTCCATCCTATGGGGACAGGAGCCTCAGGACTGCTGCCCTGCC
TGGCCCAACCTGCTCCCTCAGGTGCTGGCAGTCACCTCTGTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGGAAGGCCAGTGGAGGAGGCCAGGATGGAGAGGCCCTGGGTGCTGTGGGCCCTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTCAGGCCTGTGGGGAGTTCCGGGTGCTTATTCTTCTAAGGAAAAAAATGATAAAAT
CTCAAAGCTGATTTCTGTTAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

0 200 400 600 800 1000

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLQLQNNQLEKITYPEELSRLHRLETNLQNNRLTSRGLPEKAFLTNLYLYLANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLISSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRTMILHNQITGIGREDFATTYF
LEELNLSYNRITSPOVHRDAFRKLRLLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCCGCAGCAGACCTGCTCCGGCGCGCCCTGCCCTGTCCCTCCGGGAGCGGCAG
CACTAGCCGGCGCGAGGGCTGGGGTTCCTCGAGACTCTCAGAGGGCGCTCCCCTCGCGCCACCACCC
CAACCTGTTCTCGCGCCACTCGCTGCCAGGACCGCTGCCAACATGGATTCTCTGGCTGGCAG
GCTGGTATCTCGCTCACCTGCAGGGCGCCGAGTCAGCGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCTATGCTTATGGTGGAGGATTGACTGCTGCTGGGCTGGCTGCCAGTCTGGGACAGTGTAGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGCCAAACAAGTGCAAGTGTATCTGGTTATGGT
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGGCCGCGCTGTAAAGCAGGTGATGAAACACTTA
CGGCAGCTACAAGTGTACTGCTCACGGATATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG
CTCCATGCCAACACTGCTGATGGCTGTGATGTTAAAGGCAAATACGGTCCAGTGCCCATCCCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGATGATGTTAAAGGCTCCTGCCCTAGATT
TAGGAATGTGTCACACTTTGGAGCTACATGCAAGTGTCAATGGTCAGTATCAGTGAGCAGCTTGCTCGATGTTAA
CAAATATCAATGTATGACATAGACCAATGCTCACTGGTCAGTATCAGTGAGCAGCTTGCTCGATGTTAA
CGTACGTTGGCTCTACAAGTCAAATGTAAGAAGGATAACAGGGTGTGGACTGACTTGTTGTTAA
AGTTATGATTGAAACCTTCAGGTCATGTACCAAAGGAAATGGTACCATTTAAAGGGTGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGAAGTACTTGGCTCCGAAGACACCATATATTCTCTATCATTACCAA
CAGGCCTACTCTAAGCCAACAACAGACCTACACCAAAAGCCAACACCAATTCTACTCCACCAACACCAC
CCTGCCAACAGAGCTCAGAACACCTTACCCACCTACAACCCCCAGAAAGGCCAACCCGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACGCCCTCAGAAACCCAGAG
AGATGTGTTAGTGTCTGGTACACAGTTGATTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAGGCCAG
GGGAAAAGCTGCACGCTTGGTGTACCTCTCGGCCGCTCATGCATTAGGGACCTGTGCTGTATTCAAGGCA
CAAGGTGACGGGGCTGACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTCCACGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAATGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAAACATTGATGGTTTCAAGTATATGAGGGTGGCACAGAGAGGGTGGGACAGCTG
TTCTCCATATGCACTAAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GGCATTGTTAGAATACTCTATAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
TAAAATTTGCTTATTAAGATGGTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTCTCAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAGTAAAATCTTAACTAAATTGGACAAGGCTTAATTAGG
CAATTCCCTCTGACCTCTAACGGAGGGATTGAAAGGGGAAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCCTAGCAGTATTAAAGAAAAGGAAACTATTCTTAACTGGTAAAGGTATAAGGC
AGATATTCTAGTATCTCAGTAATGTTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGGC
TTTCATTGTTCAATGGATGATGTTCAGATTCTTAAAGAGATCCTCAAGGAACACAGTTCAAGAGAG
ATTTTCATCGGGTGCATTCTCTGTTCTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGCC
ACACCGGCAGACCTTCTTCACTCATCAGTATGATTCTCTTCAATTGGACTCTCCAGGGTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCAATTAACTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAAGCCTTGGAGTAACGGCAGAATATATGGCTGTAGATCCATTAAATGGTCATT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTCTTCAATTGGTAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAATGGCTAATAAAAACAATTATGTAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVF SVLVHSCNF DHLGCGWI REKDNDLHW EPIRD PAGGQYLT VSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHS GTLQVFVRKHGAHGA ALWGRNGGHGWRQ TQI
TLRGADIKSE SQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCACAGGTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCA
CACAAATGCCAAATACTTA~~CTGGCT~~TGTGAATAAGTCTGTGGTTCTGACTTGGAAATACC
AACACAAGTTACCATGATGCCACCCAA~~TGCATCTG~~CTTACCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCA~~GGGAA~~ATGGAAC~~TCTATCTGCCAGTCA~~
GAAGATACAAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATT~~CATCCTCCCT~~
CTGGGCTGTGGAGTATGTGGGAACATGACCC~~TGACATGCCATGTGG~~AAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGGAGGAACCTGTCA~~GATGAAATGGAAAGT~~GATATCATTATGCCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGT~~TACTGT~~
TGACCTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCC~~AAACACCTACT~~
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGCCTCGTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAA~~CATAAC~~
CGGCAGGCAAGATGAAACTCATT~~CACAGTT~~TATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCAT~~TGTAC~~CTTAGCAAGTATAACTGGAATATCACTATT~~TTT~~GATT
ATATCCATGTGCTTCTCTTCTATGGAAAAAAATCAACCC~~TACA~~AAAGTTAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAAATATGAATTGTTGCTTCCAGATGTTCTGGT~~GTT~~CCAGG
ATTCCAAGCAGGTCTG~~TCAG~~CCCTGATTGTGATCGGGCAAGATTG~~CACAGTACAGT~~
GTATGAAGTTATT~~CAGCACATCC~~CTGCCAGCAGCAAGACC~~ATCCAGAGT~~GACTT~~CATGG~~
GCTAAACAGTACATT~~CGAGT~~GAAATTCTGAAGAAACATT~~TAAGG~~AAAACAGTGGAAAAGT
ATATTAATCTGGAAATCAGTGAAGAAACCAGGCCAACAC~~CTCTTACTCATTATT~~CC~~TTT~~TACA
TGCAGAAATAGAGGCATTATGCAAATTGA~~ACTGCAGG~~TTTCAGCATATACACAA~~ATGTCTT~~
GTGCAACAGAAAAACATGTTGGGAAATATT~~CCTCAGTGGAGAGT~~CGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCAT~~AAGTTG~~TATGAAATATCTACAAAC~~CTCA~~
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATC~~TGTCTCAC~~CTACAA
TGTGGAAACTTACATTGTTG~~CAGCAGA~~CTTGT~~TTTATTAA~~ATT~~TTTATTAGT~~G
TTAAGAATGCTAAATT~~TATGTT~~CAATT~~TTTCAAA~~ATT~~TCTATCTGTTATTG~~TACAA
CAAAGTAATAAGGATGGTGT~~CACAAAA~~ACAAACTATGCC~~TTCTCTT~~TTTCAATCACC
AGTAGTATT~~TTTGAGAAGACTTGT~~GAACACTTAAGGAAATGACTATTAAAGTCTTATT~~TTTA~~
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATT~~CTGTTTTG~~CTT~~TTTAA~~AAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDPCSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGTGCTCCCTGGACGCACGGCGGCGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCCTGCT
TGTAAAATCTTCAACCGGAATGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAGAGTATTGAGCCGTTCATCATG
GTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCAGCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTGGATTGCCAGTGTGGGGATCATATACT
GTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT
TATTATCAGAATCTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCCGATGAAGAA
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTGGTCCATCATTGGCACAGATAAACTCTAGTTAAATTTATAG
TTATCTTAATATTGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAAGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTTACAAAGTTGAAATTGATTAAGCACAGTATGATG
GTTAAATAGTTCTCTAATTGAAAAATCGTCCAAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTTGAAAATTTACATTTTCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTAGAGAAAATTTCTCATTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCAGTGACAATTTCGTGGTCTTTAGAGGTATTCCAAAATTCCCTGT
ATTTTTAGTTATGCAACTAAAAACTACCTTACATTAATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAGTTCAGGGTATTCTTGATTC
CAACAAAAGTTGATTTCTCTTGATTTCTTACTTACTATGGGTACATTTTTATTTTGTT
CAAATTGGATGATAATTCTTGAAACATTTTATGTTTTAGTAAACAGTATTTTTGT
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTTAATTAAAATT
TTGGCCACTTTTCAGATTTACATCATTCTGCTGAACTTCAACTGAAATTGTTTTT
TTCTTTGGATGTGAAGGTGAACATTCCTGATTTTGTGATGTGAAAAGCCTGGTA
TTTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTTCTTGATATGCTTAAATGTATTTTTGCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTAAAATAACATTTTATTTTTAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATTTTGTGGGGATTTCACAGGAAA
GTCAGTAGGATGGAACATTTAGTGTATTTTACTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAATACAATGAATCACTGACCATTACGTAGAGAC
AATTCTGTAATGCCCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATACACAGTTCTTAAAGCCCTCCTTAGAATTAAAATTGTACCATT
AAAGAGTTGGATGTGTAACTTGTGATGCCTTAAGAAAATACCTAAGCACAAAAACCT
TTCTAACCACTCATTAAAGCTGAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

FIGURE 116

MKLWVSALLMAWFGVLSHVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVYDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYVGQQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTGGCTGGGGTTAGTCCGACACCTTCACAGTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTCTGGGATGCTGGTCTTGAAGCCAGCGGGCCTTGCCTGTCTTGGCCTCATGACCC
CAGGTTCTCTGGTAAAGCTACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCCTACCAATGCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTGGGGTGCAGCCTGAGCCTCCTGCCGGTTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGGTGCTGGCTGTGACCTCCCGAGGCTACACTGTCCA
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTGGTTACTCTACTTCACTGGCAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGGCCTGGCTCATGTCAGAGAACCCCTGC
GCCACCTTCACACACACTTGGGGCCGACTACGACTGGTTCTCATCATGCAGGATGACACATATGTGAGGCC
CCCGCCTGGCAGCCCTTGTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTATTG
GCGCAGCGAGCAGGCCGGTACTGTCTGGGGCTTGGTACCTGTGACGGAGTCTCCTGCTCGTGC
GGCCACATCTGGATGGCTGGCAGGGAGACATTCTCAGTGGCCGTCTGACGAGTGGCTGGACGCTGCCATTG
ACTCTCTGGGCGTGGCTGTGTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACGGCCAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTCGGTTCTGAGTGCCTCGCGTGCACCGTCTCCGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTTGGAGTTGGAGCGGGCTTACAGTGAACATAGAACAACTGAGGCTCAGA
TCCGGAACCTGACCGTGCTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGGTGGCTCCCTGCTCCATTCA
CACCAACACTCGCTTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTTCTCTGTGAGATGGGG
CTCCCAAGTGCCACTACAGGGGGTAGCAGGGGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGGCCTATCAGCCCCGCTCGCCTCCAGAACGAGCAGCAGTGCACCGCTATCGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCTGGACCTGCTGTTGGAAATGTGTGACACAGCGTGGGACCGGGCCCTGGCTCGCA
GGGTCAAGCCTGCTGCGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGCCATGTCC
TGGAGGCCAGAGAACATGCATTGCTACCCGTGCTGGTCTACGGGGCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAAGCAGCGGAGTTAGAGCAGCGTACCCCTGGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCACTCATGGACGCTGGCTCGAAGAACGACCCCTGTGGACACTCTCT
TCTTCCCTTACCAACCGTGTGGACAAGGCCCTGGGCCGAAGTCCCTCAACCGCTGCGCATGAATGCCATCTGGCT
GGCAGGCCCTTCTCCAGTCCATTCCAGGAGTTCAATCCCTGGCCCTGTGACCCAGAGATCACCCCCAGGGGG
CGGGGGCTGGCCCTGACCCCCCTCCCTGGCTGCTGACCCCTCCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCCCTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGCCAGCCCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGGAGGAAGGCCCTGGAGGGCTGGAGGTGATGGATGTTTCCTCCGGTTCTCAGGGCTCC
ACCTCTTCCGGCCGTAGAGGCCAGGGCTGGTGCAGAACGTTCTCCCTGCGAGACTGCAAGCCCACGGCTCAGTGAAG
AACTCTACCACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCGTGCCTAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGCCCTAACCTCATACCTTCTGTGCTGCCCTAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMETYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLVVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVTRPGPEVLRNCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACGTGAGAGGAACCGTGCACGGCTGCCTTCCTGCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTTGGCATATTTCAAT
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTTGAGAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGCATTATTGTAGTAGTAACATACATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCCTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTGTAAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCAGTGCCTGTTCATCACCAAGATGTGTTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAGTTCAGCTACCTGAGAATTTCACAGAGCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGCCATTGAACGGAAATTTCATCC
AGCTGCTACTTCTTTCTACTGACACCATTCCGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGCCAAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTCGGATTGTGAAATGGTAGGAATAAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAACGGACAACCTCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATAACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPIFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCCGCGCCGCTGCCGCTGGCCCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCGGCTCTGCGCTCGGCTGACTTCTTCTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCCTGCATCATTACGGATTGC
AGACAAGTGACCCCAAGGATCGAGTGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGGCGAAGGCTGTACCGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGCCACCCCCGGCCTACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGCACCTGGTGTACTGCTG
TTCACAAGGAGACTCTGGCAGTACTACTGCATTGCTTCCAATGACCGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTTGCTCTGCTGACTGGCCCTGA
TCACCTGGGCATCTGCTGTGCATAACAGACGTGGCTACTTCATCAAAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGGCAGACTCAGACAAAGTCATCGTTG
TGATCTGAGACCCCGGGTGGCTGAGAGCGCACAGGCGCACGTGACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTGACACTCATTCAAGGCTTTCGTTGGCCAAAGTTGACCA
CTACTCTTCTACTCTAACAGGACATGAATAGAAGAATTCTCTCAAGATGGACCCGGTAAATAACACCAA
GGAAGCGAAACTGGGTGGCTTACTGAGTTGGCTTAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTAAAGAGTTGCTCACGTAACAGGACATGTGAGATGGCGAGGTGGACAGCACCAGCAGCGCATCCGGGGAAACCA
GAAAAGGCTTCTACACAGCAGCTTACTCTCATGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTTGAGTGTCCATTGGAGAAGCTTTGGATCAGCATTGTAAGGAAACACAAAATCAGGAAG
GTAAATTGGTGTGAGGAGGATCTGCTGAGGAACCTGCTGTCCAACAGGGTGTAGGATTTAAGGAA
ACCTCGTCTTAGGCTAACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTGTTATTTATAAAATT
TACATCTAAATTGGTAAAGGATGTATTGATTATTGAAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGTAAAGGTTCAACTTAAGGTAGAAGTCCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTGACCGAACTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTAGCCTTTTCAAGGAAACTCATACTGTCACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCTCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCTGAGATGACTAGGACAGCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACACACAGATG
CCAGTCAGCTCTGGGGTGGCCAGGGCCCCCGCTAGCTACTGTTGCTCCGCTGCTGCCAGGGCCCT
GCCATCCTGGGCCCTGGCAGTGGCTGTCTCCAGTGTAGCTTACTCACGTGGCCCTGCTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGACACTGGTGTCTCCATGTAGCTGCTCCAGTGTGCTTAACAGACCTCT
TTTGGTTATGGCTCACAAATAGGGCCCCCAATGCTATTGTTTAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCCAAGGCAATTGCAAATCAAGTGTCAAGTACAATAACATTGTTAAAGAAAATGGAT
CCCACGTGTTCTTTGCACAGAGAAAGCACCAGCAGCAGGCTCTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCAGGCTGAAAGGCTGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTAAATTGTTCATCCGCCGGAGACACTGCTCCATT
TGTGGGGGGACATTGCAACATCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCAGTCCACTGTGTGCCCTGGA
GAATGGCTCTCACTACTCACCTGCTTTCAGCTTCCAGTGTCTGGTTTTTATACCTTGACAGCTTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTTTAGTTATGTGAAACACTTGCCTGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATTCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCACTGCTCCAGCCTCCT
TCTGGTTGTCATAGTGTAGGGTAGCCTTATTGCCCTCTTACCTAAACCTCTACACTAGTGCCTA
TGGGAACCCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCCTAAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAHYRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267